

In the Specification:

Please amend the paragraph beginning at page 5, line 20 of the specification as follows:

--The sequences of the MHC class I and II cDNAs and genomic DNAs are published and available (~~www.ncbi.nlm.nih.gov/Genbank~~).--

Please amend the paragraph beginning at page 11, line 6 of the specification as follows:

--Some of the MHC claim I, like HLA A2, are expressed in more than 20% of the population. In circumstances where a MHC negative cell line is used, one or more than one compatible MHC gene is transfected into the cell line by means of conventional gene transfer methods and the transgene is constructed into a expression vector. The expression cassette of expression construct normally includes standard promoter, such as CMV promoter, or elongation factorI promoter or actin promoter, enhancer, inserted transgene and the poly-A signal to achieve optimal expression. Before transfection, the expression cassette will be isolated from the plasmid backbone to avoid the expression of bacterial plasmid genes in transfected cells. The sequences of the MHC class I and II cDNAs and genomic DNAs are published and available (~~www.ncbi.nlm.nih.gov/Genbank~~). A MHC class I transfectants Bank can be constructed by using MHC class I negative or selected MHC class positive cell lines to transfect most of the MHC class I genes, respectively. The selection of the expression cassette will be dependent on the optimal expression of the transgene.--

Please amend the paragraph beginning at page 21, line 14 of the specification as follows:

--The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul Proc. Natl. Acad. Sci. USA (1990) 87:2264-2268, modified as Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. The NBLAST and XBLAST programs of Altschul et al, J. Mol. Biol. (1990) 215:403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide

sequences homologous to a nucleic acid molecules encoding a peptide sequence as described herein. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a peptide as described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilised as described in Altschul et al, Nucleic Acids Res. (1997) 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PST-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~See, for example,~~ <http://www.ncbi.nlm.nih.gov>--